RAW SEQUENCE LISTING ERROR REPORT
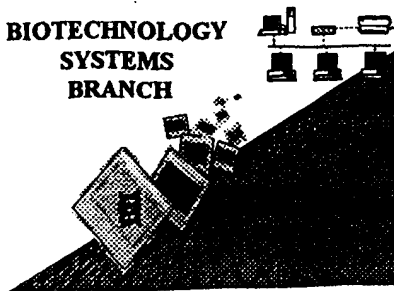
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED

Application Serial Number: _09/068, 253_

MAR 0 5 2001

Source: _1653_

TECH CENTER 1600/2900

Date Processed by STIC: _2/26/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

SERIAL NUMBER: _09/068,253_

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MAR 0 5 2001

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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

(J. Moezie)

RAW SEQUENCE LISTING   DATE: 02/26/2001
PATENT APPLICATION: US/09/068,253   TIME: 16:41:00

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: SHIMURA, Takesada
 4        TORIYAMA, Satsuki
 6 <120> TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
 8 <130> FILE REFERENCE: 146.1286
10 <140> CURRENT APPLICATION NUMBER: 09/068,253
11 <141> CURRENT FILING DATE: 1998-06-09
13 <150> PRIOR APPLICATION NUMBER: PCT/JP96/03333
14 <151> PRIOR FILING DATE: 1996-11-14
16 <150> PRIOR APPLICATION NUMBER: JP 7/322402
17 <151> PRIOR FILING DATE: 1995-11-17
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 357
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(357)
31 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO: 1 from
32        1 to 119 in WO 95/04819
34 <300> PUBLICATION INFORMATION:
35 <301> AUTHORs: HOTTEN, Gertrud
36        NEIDHARDT, Helge
37        PAULISTA, Michael
38 <302> TITLE: NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF-BETA
39        FAMILY
40 <310> PATENT DOCUMENT NUMBER: WO 95/04819
41 <311> PATENT FILING DATE: 1995-02-16
42 <313> RELEVANT RESIDUES: 1 TO 119
44 <400> SEQUENCE: 1
45 cca ctg gcc act cgc cag ggc aag cga ccc agc aag aac ctt aag gct    48
46 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
47  1               5                   10                  15
49 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg    96
50 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
51              20                  25                  30
53 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag   144
54 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
55          35                  40                  45
57 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat   192
58 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
59          50                  55                  60
61 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca   240
62 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
63  65                  70                  75                  80
65 ccc acc tgc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc   288
```

W--> (handwritten annotation): give the serial number of the filed application, not the issued patent number (see 1.823 of new Sequence Rules)

pp 1-2

RAW SEQUENCE LISTING   DATE: 02/26/2001
PATENT APPLICATION: US/09/068,253   TIME: 16:41:00

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

```
66 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
67             85              90              95
69 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc   336
70 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
71             100             105             110
73 gtg gag tcg tgt ggc tgc agg                                      357
74 Val Glu Ser Cys Gly Cys Arg
75             115
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 119
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 2
84 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
85   1           5               10              15
87 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
88             20              25              30
90 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
91             35              40              45
93 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
94       50              55              60
96 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
97 65              70              75              80
99 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
100             85              90              95
102 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
103            100             105             110
105 Val Glu Ser Cys Gly Cys Arg
106            115
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 27
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence:
117      oligonucleotide
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(27)
122 <223> OTHER INFORMATION: PCR forward primer for isolating mature-type MP52
124 <400> SEQUENCE: 3
125 ataatgccac tagcaactcg tcagggc                                    27
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 26
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:
135      oligonucleotide
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(handwritten) → invalid response — give source of genetic material — (see circled portion of item 12 on Error Summary sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/068,253

DATE: 02/26/2001
TIME: 16:41:00

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: Complement((1)..(26))
140 <223> OTHER INFORMATION: PCR reverse primer for isolating mature-type MP52
142 <400> SEQUENCE: 4
143 cgtcgactac ctgcagccac acgact   26

VERIFICATION SUMMARY   DATE: 02/26/2001
PATENT APPLICATION: US/09/068,253   TIME: 16:41:01

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

L:40 M:256 W: Invalid Numeric Header Field, Wrong PATENT DOCUMENT NUMBER:US NN/NNN,NNN